

OIEP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/837,961

DATE: 05/08/2001
TIME: 15:59:31

#2
ENTERED

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Output Set: N:\CRF3\05082001\I837961.raw

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3 <110> APPLICANT: Payne, Jewel
4   Sick, August
6 <120> TITLE OF INVENTION: Novel Bacillus thuringiensis Isolate Active Against Lepidopteran Pests,
7   and Genes Encoding Novel Lepidopteran-Active Toxins
9 <130> FILE REFERENCE: MA-43CDF2D3
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/837,961
C--> 11 <141> CURRENT FILING DATE: 2001-04-19
11 <150> PRIOR APPLICATION NUMBER: US 09/521,344
12 <151> PRIOR FILING DATE: 2000-03-09
14 <150> PRIOR APPLICATION NUMBER: US 08/933,891
15 <151> PRIOR FILING DATE: 1997-09-19
17 <150> PRIOR APPLICATION NUMBER: US 08/356,034
18 <151> PRIOR FILING DATE: 1994-12-14
20 <150> PRIOR APPLICATION NUMBER: US 08/210,110
21 <151> PRIOR FILING DATE: 1994-03-17
23 <150> PRIOR APPLICATION NUMBER: US 07/865,168
24 <151> PRIOR FILING DATE: 1992-04-09
26 <150> PRIOR APPLICATION NUMBER: US 07/451,261
27 <151> PRIOR FILING DATE: 1989-12-14
29 <150> PRIOR APPLICATION NUMBER: US 371,955
30 <151> PRIOR FILING DATE: 1989-06-27
32 <160> NUMBER OF SEQ ID NOS: 8
34 <170> SOFTWARE: PatentIn version 3.0
36 <210> SEQ ID NO: 1
37 <211> LENGTH: 3528
38 <212> TYPE: DNA
39 <213> ORGANISM: Bacillus thuringiensis
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46 caattttctgt tgagtgaatt tgtcccaggt gctgggtttg tattagggtt aattgattta      180
48 atatgggggt ttgtgggtcc ctctcaatgg gatgcatttc ttgtgcaaat tgaacagtta      240
50 attaaccaaa gaatagagga attcgctagg aaccaagcaa tttctagatt agaagggcta      300
52 agcaaccttt atcaaattta cgcagaagct tttagagagt gggaagcaga tcctactaat      360
54 ccagcattaa cagaagagat gcgtattcag ttcaatgaca tgaacagtgc tcttacaacc      420
56 gctattcctc tttttacagt tcaaaattat caagtacctc ttctatcagt atatgttcaa      480
58 gctgcaaatt tacattttatc ggtttttgaga gatgtttcag tgtttggaca acgttgggga      540
60 tttgatgtag caacaatcaa tagtcgttat aatgatttaa ctaggcttat tggcacctat      600
62 acagattatg ctgtacgctg gtataatacg ggattagaac gtgtatgggg accggattct      660
64 agagattggg taagggtataa tcaatttaga agagagctaa cactaactgt attagatatc      720
66 gtttctctgt tcccgaacta tgatagtaga acgtatccaa ttcgaacagt ttcccaatta      780
68 actagagaaa ttatatacaa ccagtatta gaaaattttg atggtagttt tctgtggaatg      840
70 gctcagagaa tagaacagaa tattaggcaa ccacatctta tggatctcct taatagtata      900
72 accattttata ctgatgtgca tagaggcttt aattattggt caggacatca aataacagct      960
74 tctcctgtcg gttttgcggg gccagaattt acttttcccta gatattggaac catgggaaat      1020
76 gctgctccac ccgtactgat ctcaactact ggtttgggga tttttagaac attatcttca      1080
78 cctctttaca gaagaattat acttggttca ggcccaaata atcagaacct gtttgtcctt      1140

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80 gatggaacgg aattttcttt tgctcccta acagccgatt taccttctac tatatacaga 1200
82 caaaggggaa cggtcgattc actagatgta ataccgccac aggataatag tgtgccagca 1260
84 cgtgcgggat ttagtcatcg attaatgcat gttacaatgc tgagccaagc agctggagca 1320
86 gtttacacct tgagagctcc aacgttttct tggcgacatc gtagtgctga attctctaac 1380
88 ctaattcctt catcacaaat cacacagata cctttaacaa agtctattaa tcttggtctt 1440
90 gggacctctg ttgttaaagg accaggatgt acaggaggag atattcttcg aataacttca 1500
92 cctggccaga tttcaacctt aagagtgact attacggcac cattatcaca aagatatcgc 1560
94 gtaagaattc gctacgcttc tactacaaat ttacaattcc atacatcaat tgacggaaga 1620
96 cctattaatc aggggaatgt ttcagcaact atgagtagtg ggggtaattt acagtcggga 1680
98 agcttttaga ctgcagggtt tactactccg tttactttt caaatggatc aagtatatat 1740
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102 gttccggcag aagtaacatt tgaggcggaa tatgatttag aaagagcgca agaggcggg 1860
104 aatgctctgt ttacttcttc caatcaacta ggattaaaaa caaatgtgac ggactatcat 1920
106 attgatcaag tgtccaatct agtcgaatgt ttatccgggt aattctgtct ggatgaaaag 1980
108 agagaattgt ccgagaaagt caaacatgcg aaccgactca gtgatgagcg gaatttactt 2040
110 caagacccaa acttcagagg catcaataga caaccagacc gtggctggag aggcagtacg 2100
112 gatattacca tccaaggagg agatgacgta ttcaaagaga attacgtcac actaccgggt 2160
114 acctttaatg agtggtatcc tacgtatctg ttcaaaaaa tagatgagtc gaaattaaaa 2220
116 gcctataccc gttaccaatt aagagggtag atcgaggata gtcaacactt agaaatctat 2280
118 ttaattcgct acaatacaaa acacgaaaca gtaaatgtgc caggtagcggg ttccttatgg 2340
120 ccgctttcag tcgaaaatcc aattggaaag tgcggagaac caaatcgatg cgcaccacaa 2400
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124 tcccatcatt tctccttgga cattgatatt ggatgtacag atttaaatga gaacttaggt 2520
126 gtatgggtga tattcaaaat taagatgcaa gatggtcacg caagactagg taatctagag 2580
128 tttctcgaag agaaaccatt agtaggcgaa tcgttagcac gcgtgaagag agcggagaag 2640
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132 aaagaatctg tagatgcttt atttgtgaac tctcaatatg atagattaca agcggatacc 2760
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136 ccagagttat ctgtaattcc ggggtgtcaat gcgggcatgt ttgaagaatt agagggacgt 2880
138 attttcacag cctactcttt atatgatgcg agaaatgtca ttaaaaatgg cgatttcaat 2940
140 aatggcttat catgctggaa cgtgaaaggg catgtagatg tagaagaaca aaacaaccac 3000
142 cgttcgggtc ttgtgttccc ggaatgggaa gcagaggtgt cacaagaggt tcgtgtctgt 3060
144 ccaggtcgtg gctatatcct acgtgttaca gcgtacaaag agggatatgg agaaggttgc 3120
146 gtaacgattc atgagatcga agacaatata gacgaactga aattcagcaa ctgtgtagaa 3180
148 gaggaagtat atccaaacaa cacggtaacg tgtaatgatt atactgcaa tcaagaagaa 3240
150 tacgggggtg cgtacacttc tcgtaatcgt ggatatggtg aatcttatga aagtaattct 3300
152 tccataccag ctgagtatgc gccagtttat gaggaagcat atatagatgg aagaaaagag 3360
154 aatccttgtg aatctaacag aggatatggg gattacacgc cactaccagc tggttatgtg 3420
156 acaaaagaat tagagtactt ccagaaaacc gataaggtat ggattgagat cggggaaacg 3480
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161 <210> SEQ ID NO: 2

162 <211> LENGTH: 1176

163 <212> TYPE: PRT

164 <213> ORGANISM: Bacillus thuringiensis

166 <400> SEQUENCE: 2

168 Met Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu Asn Asp Pro

169 1 5 10 15

171 Thr Ile Glu Ile Leu Glu Gly Glu Arg Ile Glu Thr Gly Tyr Thr Pro

172 20 25 30

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174 Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser Glu Phe Val
175           35           40           45
177 Pro Gly Ala Gly Phe Val Leu Gly Leu Ile Asp Leu Ile Trp Gly Phe
178           50           55           60
180 Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu Gln Leu
181 65           70           75           80
183 Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala Ile Ser Arg
184           85           90           95
186 Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu Ala Phe Arg
187           100          105          110
189 Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Thr Glu Glu Met Arg
190           115          120          125
192 Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala Ile Pro Leu
193           130          135          140
195 Phe Thr Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val Tyr Val Gln
196 145          150          155          160
198 Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser Val Phe Gly
199           165          170          175
201 Gln Arg Trp Gly Phe Asp Val Ala Thr Ile Asn Ser Arg Tyr Asn Asp
202           180          185          190
204 Leu Thr Arg Leu Ile Gly Thr Tyr Thr Asp Tyr Ala Val Arg Trp Tyr
205           195          200          205
207 Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg Asp Trp Val
208           210          215          220
210 Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val Leu Asp Ile
211 225          230          235          240
213 Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro Ile Arg Thr
214           245          250          255
216 Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val Leu Glu Asn
217           260          265          270
219 Phe Asp Gly Ser Phe Arg Gly Met Ala Gln Arg Ile Glu Gln Asn Ile
220           275          280          285
222 Arg Gln Pro His Leu Met Asp Leu Leu Asn Ser Ile Thr Ile Tyr Thr
223           290          295          300
225 Asp Val His Arg Gly Phe Asn Tyr Trp Ser Gly His Gln Ile Thr Ala
226 305          310          315          320
228 Ser Pro Val Gly Phe Ala Gly Pro Glu Phe Thr Phe Pro Arg Tyr Gly
229           325          330          335
231 Thr Met Gly Asn Ala Ala Pro Pro Val Leu Ile Ser Thr Thr Gly Leu
232           340          345          350
234 Gly Ile Phe Arg Thr Leu Ser Ser Pro Leu Tyr Arg Arg Ile Ile Leu
235           355          360          365
237 Gly Ser Gly Pro Asn Asn Gln Asn Leu Phe Val Leu Asp Gly Thr Glu
238           370          375          380
240 Phe Ser Phe Ala Ser Leu Thr Ala Asp Leu Pro Ser Thr Ile Tyr Arg
241 385          390          395          400
243 Gln Arg Gly Thr Val Asp Ser Leu Asp Val Ile Pro Pro Gln Asp Asn
244           405          410          415
246 Ser Val Pro Ala Arg Ala Gly Phe Ser His Arg Leu Ser His Val Thr

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247		420		425		430
249	Met Leu, Ser	Gln Ala Ala Gly	Ala Val Tyr Thr	Leu Arg Ala Pro	Thr	
250		435		440		445
252	Phe Ser Trp	Arg His Arg Ser	Ala Glu Phe Ser	Asn Leu Ile Pro	Ser	
253		450		455		460
255	Ser Gln Ile	Thr Gln Ile Pro	Leu Thr Lys Ser	Ile Asn Leu Gly	Ser	
256	465		470		475	480
258	Gly Thr Ser	Val Val Lys Gly	Pro Gly Phe Thr	Gly Gly Asp Ile	Leu	
259		485		490		495
261	Arg Ile Thr	Ser Pro Gly Gln	Ile Ser Thr Leu	Arg Val Thr Ile	Thr	
262		500		505		510
264	Ala Pro Leu	Ser Gln Arg Tyr	Arg Val Arg Ile	Arg Tyr Ala Ser	Thr	
265		515		520		525
267	Thr Asn Leu	Gln Phe His Thr	Ser Ile Asp Gly	Arg Pro Ile Asn	Gln	
268		530		535		540
270	Gly Asn Phe	Ser Ala Thr Met	Ser Ser Gly Gly	Asn Leu Gln Ser	Gly	
271	545		550		555	560
273	Ser Phe Arg	Thr Ala Gly Phe	Thr Thr Pro Phe	Asn Phe Ser Asn	Gly	
274		565		570		575
276	Ser Ser Ile	Phe Thr Leu Ser	Ala His Val Phe	Asn Ser Gly Asn	Glu	
277		580		585		590
279	Val Tyr Ile	Glu Arg Ile Glu	Phe Val Pro Ala	Glu Val Thr Phe	Glu	
280		595		600		605
282	Ala Glu Tyr	Asp Leu Glu Arg	Ala Gln Glu Ala	Val Asn Ala Leu	Phe	
283		610		615		620
285	Thr Ser Ser	Asn Gln Leu Gly	Leu Lys Thr Asn	Val Thr Asp Tyr	His	
286	625		630		635	640
288	Ile Asp Gln	Val Ser Asn Leu	Val Glu Cys Leu	Ser Gly Glu Phe	Cys	
289		645		650		655
291	Leu Asp Glu	Lys Arg Glu Leu	Ser Glu Lys Val	Lys His Ala Asn	Arg	
292		660		665		670
294	Leu Ser Asp	Glu Arg Asn Leu	Leu Gln Asp Pro	Asn Phe Arg Gly	Ile	
295		675		680		685
297	Asn Arg Gln	Pro Asp Arg Gly	Trp Arg Gly Ser	Thr Asp Ile Thr	Ile	
298		690		695		700
300	Gln Gly Gly	Asp Asp Val Phe	Lys Glu Asn Tyr	Val Thr Leu Pro	Gly	
301	705		710		715	720
303	Thr Phe Asn	Glu Cys Tyr Pro	Thr Tyr Leu Tyr	Gln Lys Ile Asp	Glu	
304		725		730		735
306	Ser Lys Leu	Lys Ala Tyr Thr	Arg Tyr Gln Leu	Arg Gly Tyr Ile	Glu	
307		740		745		750
309	Asp Ser Gln	His Leu Glu Ile	Tyr Leu Ile Arg	Tyr Asn Thr Lys	His	
310		755		760		765
312	Glu Thr Val	Asn Val Pro Gly	Thr Gly Ser Leu	Trp Pro Leu Ser	Val	
313		770		775		780
315	Glu Asn Pro	Ile Gly Lys Cys	Gly Glu Pro Asn	Arg Cys Ala Pro	Gln	
316	785		790		795	800
318	Leu Glu Trp	Asn Pro Asp Leu	Asp Cys Ser Cys	Arg Asp Gly Glu	Lys	
319		805		810		815

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321 Cys Ala His His Ser His His Phe Ser Leu Asp Ile Asp Ile Gly Cys
322      820      825      830
324 Thr Asp Leu Asn Glu Asn Leu Gly Val Trp Val Ile Phe Lys Ile Lys
325      835      840      845
327 Met Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu
328      850      855      860
330 Lys Pro Leu Val Gly Glu Ser Leu Ala Arg Val Lys Arg Ala Glu Lys
331 865      870      875      880
333 Lys Trp Arg Asp Lys Arg Glu Lys Leu Gln Val Glu Thr Asn Ile Val
334      885      890      895
336 Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln
337      900      905      910
339 Tyr Asp Arg Leu Gln Ala Asp Thr Asp Ile Ala Met Ile His Ala Ala
340      915      920      925
342 Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser
343      930      935      940
345 Val Ile Pro Gly Val Asn Ala Gly Ile Phe Glu Glu Leu Glu Gly Arg
346 945      950      955      960
348 Ile Phe Thr Ala Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn
349      965      970      975
351 Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val Lys Gly His Val
352      980      985      990
354 Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu Val Val Pro Glu
355      995      1000      1005
357 Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg
358      1010      1015      1020
360 Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu
361      1025      1030      1035
363 Gly Cys Val Thr Ile His Glu Ile Glu Asp Asn Thr Asp Glu Leu
364      1040      1045      1050
366 Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr
367      1055      1060      1065
369 Val Thr Cys Asn Asp Tyr Thr Ala Asn Gln Glu Glu Tyr Gly Gly
370      1070      1075      1080
372 Ala Tyr Thr Ser Arg Asn Arg Gly Tyr Gly Glu Ser Tyr Glu Ser
373      1085      1090      1095
375 Asn Ser Ser Ile Pro Ala Glu Tyr Ala Pro Val Tyr Glu Glu Ala
376      1100      1105      1110
378 Tyr Ile Asp Gly Arg Lys Glu Asn Pro Cys Glu Ser Asn Arg Gly
379      1115      1120      1125
381 Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu
382      1130      1135      1140
384 Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly
385      1145      1150      1155
387 Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu
388      1160      1165      1170
390 Met Glu Glu
391      1175
393 <210> SEQ ID NO: 3

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date